# STIC Search Report
## Biotech-Chem Library

**TO: Ramin Akhavan**
**Location: rem/2c84/2c70**
**Art Unit: 1636**
**Tuesday, November 23, 2004**
**Case Serial Number: 09/743347**

**From: Paul Schulwitz**
**Location: Biotech-Chem Library**
**REM-1A65**
**Phone: (571)272-2527**

**paul.schulwitz@uspto.gov**

## Search Notes

Examiner Akhavan,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

**From:** Akhavan, Ramin
**Sent:** Sunday, November 14, 2004 1:44 PM
**To:** STIC-Biotech/ChemLib
**Subject:** 09743347

**Contacts:** STIC-Biotech/ChemLib


Please conduct a standard search for the nucleotide sequence that is the complement of SEQ ID NO: 2, AND the following complementary stretches in SEQ ID NO: 2:

| | |
|---|---|
| complement to sequence stretch from position | -153 to -139 |
| """ | -46 to -35 |
| """ | -162 to -1 |
| """ | -161 to -35 |
| """ | -268 to -35 |
| """ | -83 to -1 |

Thanks very much.  Please let me know if you need any clarification.

Ray Akhavan
Patent Examiner, AU 1636        *2C70*
Remsen Building, 2C84
571-272-0766; 703-395-0410 (cell)
ramin.akhavan@uspto.gov

*s/L*

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# SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is _____.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.